SEQUENCE LISTING

5	(1) GENERAL INFORMATION:
	(i) APPLICANT:
	(A) NAME: CLOUGH et al
	(B) STREET: National Institute for Medical Research, Mill
10	Hill
	(C) CITY: London
	(E) COUNTRY: United Kingdom
	(F) POSTAL CODE (ZIP): NW7 1AA
15	(11) TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA
	OF THE MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
20	(iii) NUMBER OF SEQUENCES: 2
20	(iv) COMPUTER READABLE FORM:
	(1),
	(A) MEDIUM TYPE: Floppy disk
	(B) COMPUTER: IBM PC compatible
	(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25	(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
	(v) CURRENT APPLICATION DATA:

- 30 (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:

APPLICATION NUMBER: US NA

			(B) TY	NGTH PE: RAND	nucl	eic	acid		S							
			(D) TO	POLO	GY:	line	ar									
5		(ii)	MOL	ECUL.	E TY	PE:	DNA	(gen	omic)							
		(ix)	FEA	TURE	:												
10			(A	NA (A	ME/K	EY:	CDS										
			(B	B) LC	CATI	ON:1	12	30									
		(xi)	SEC	QUENC	E DE	SCRI	PTIC	N: S	EQ I	D NO): 1:						
15						-		•			C 4 4	CAT	4.74		TT 4	COT	40
									AAT Asn								48
	met 1	ASTI	ASTI	Lys	Leu 5	Prie	Leu	Arg	ASTI	10	GIII	піѕ	Tie	ASII	15	uly	
	-				,					10					10		
20	ACT	ATA	GGG	CAT	GTA	GAT	CAT	GGA	AAA	ACT	ACA	TTA	ACA	ACA	GCT	ATA	96
	Thr	Ile	Gly	His	۷a٦	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Thr	A٦a	Ile	
				20					25					30			
									TTA								144
25	Ser	Tyr			Asn	Leu	Gln	-	Leu	Ser	Lys	Lys		Asn	Tyr	Ser	
			35					40					45				
	GAT	ATT	GAT	TCA	CCT	CCA	GAA	GAA	AAA	ΔΤΔ	ΔGΔ	GGT	ΔΤΤ	ΔΩΔ	ΔΤΔ	ΤΔΔ	192
									Lys								
30		50			, u		55		-3.5		9	60					
	ACA	ACA	CAT	ATT	GAA	TAT	GAA	ACT	TTA	ACA	AAA	CAT	TGT	GCT	CAT	ATA	240

	Thr	Thr	His	Пe	Glu	Tyr	Glu	Thr	Leu	Thr		His	Cys	Ala	His			
	65					70					75					80		
	GAT	TGT	CCA	GGA	САТ	TCC	GAT	ТАТ	ATT	AAA	AAT	ATG	ATT	ATA	GGA	GCC	288	
5			Pro														200	
5	лор	0,0		٠.,	85					90					95			
	ACA	CAA	ATG	GAT	ATA	GCA	ATT	TTA	GTA	ATA	TCT	ATA	ATA	GAT	GGT	ATA	336	
	Thr	Gln	Met	Asp	Пe	Ala	IJе	Leu	Val	Пe	Ser	Ile	Ile	Asp	Gly	Ile		
10				100					105					110				
			CAA														384	
	Met	Pro		Thr	lyr	Glu	HIS	Leu 120	Leu	Leu	Пе	Lys	125	Пе	GIY	Ile,		
15			115					120					125					
13	AAA	ААТ	ATA	ATT	ATT	ттт	TTA	AAT	AAA	GAA	GAT	TTA	TGT	GAT	GAT	GTT	432	
			Ile															
		130					135				·	140		·				
20	GAA	TTA	ATA	GAT	Ш	ATA	AAA	TTA	GAA	GTA	AAT	GAA	TTA	TTA	ATT	AAA	480	
	Glu	Leu	Пe	Asp	Phe	Пe	Lys	Leu	G1 u	۷a۱	Asn	Glu	Leu	Leu	Ile	Lys		
	145					150					155					160		
																TTA	528	
25	iyr	Asn	Phe	Asp	Leu 165		ıyr	He	HIS	170		ıınr	GIY	ser	175	Leu		
					100					170					1/5			
	AAT	GT#	ATA A	. AAT	ATA	TTA	CAA	AAA	. AAT	AAG	GAT	TAT	GAA	TTA	ATA	AAA	576	
	Asr	ı Val	Il€	Asr	ı Ile	: Ile	e G1n	Lys	Asr	Lys	Asp	Tyr	· Glu	ı Leı	ı Ile	Lys		
30				180)				185	5				190)			
	TCT	AA 1	ГАТ	TGO	ATA £	CA/	AA.	TTA	TAA A	TAA T	Π/	A AT	CA	ATA A	TA A	GAT	624	

	ser	ASN	195	ırp	11e	GIN	Lys	200	ASN	ASN	Leu	11e	205	11e	11e	ASP		
	AAT	ATT	АТА	АТА	ССТ	ACT	AGA	AAA	ATT	AAT	GAT	TAC	Ш	TTA	ATG	TCA		672
5	Asn	Ile	Ile	Ile	Pro	Thr	-	Lys	Ile	Asn	Asp	-	Phe	Leu	Met	Ser		
		210					215					220						
	ATA	GAA	GAT	GTA	Ш	тст	ATA	ACA	GGT	AGA	GGT	ACA	GTA	GTA	ACA	GGT		720
	Ile	Glu	Asp	۷a٦	Phe	Ser	Пe	Thr	G1 y	Arg	G1 y	Thr	Val	Va1	Thr	G1y		
10	225					230					235					240		
	AAG	ATT	GAA	CAA	GGA	TGT	ATA	AAT	TTA	AAT	GAT	GAA	ATT	GAA	ATT	TTA		768
	Lys	Ile	G1 u	G1n	G1 y	Cys	Ile	Asn	Leu	Asn	Asp	G1u	Ile	G1 u	Ile	Leu		
					245					250					255			
15																		
	AAA	П	GAA	AAA	TÇA	TCT	CCT	AAT	TTA	ACA	ACA	GTT	ATA	GGA	TTA	GAA		816
	Lys	Phe	Glu	Lys	Ser	Ser	Pro	Asn	Leu	Thr	Thr	Val	Пe	G1 y	Leu	G1 u		
				260					265					270				
20	ATG	ПТ	AAA	AAA	CAA	TTA	ACA	CAA	GCA	CAA	TCC	GGA	GAT	AAT	GTA	GGT		864
	Met	Phe	Lys	Lys	Gln	Leu	Thr	G1n	A٦a	G1n	Ser	G1y	Asp	Asn	۷al	Gly		
			275					280					285					
	ATT	ΤΤА	TTA	AGA	AAT	ATT	CAA	AAA	AAA	GAT	ATA	AAA	AGA	GGT	ATG	ATT		912
25	Ile	Leu	Leu	Arg	Asn	Ile	G1n	Lys	Lys	Asp	Ile	Lys	Arg	G1 y	Met	Ile		
		290					295					300						
																,		
		GCA																960
		Ala	Thr	Pro	Asn	-		Lys	Val	Tyr	•		Phe	Ile	Ala			
30	305					310					315					320		
	ACA	TAT	ATT	ТТА	ACT	AAA	GAA	GAA	GGT	GGT	CGT	CAT	AAA	ССТ	Ш	AAT	1	80 0 1

	Thr	Tyr	Пe	Leu	Thr	Lys	G1 u	G1 u	Gly	Gly	Arg	His	Lys	Pro	Phe	Asn	
				•	325					330					335		
	ATT																1056
5	Ile	G1y	Tyr		Pro	G1n	Phe	Phe		Arg	Inr	Val	Asp		ınr	GIY	
				340					345					350			
	GAA	ATT	AAA	AAT	ATA	TAT	TTA	AAT	GAA	AAT	GTA	CAA	AAA	GTA	GCT	ATA	1104
	G1u	Пe	Lys	Asn	He	Tyr	Leu	Asn	Glu	Asn	۷a٦	G1 n	Lys	Va1	Ala	Пе	
10			355					360					365				
	CCT	GGA	GAT	AAA	ATA	ACA	TTA	CAT	ATT	GAA	ΠA	AAA	CAT	TAT	ATA	GTG	1152
	Pro	G1 y	Asp	Lys	Пe	Thr	Leu	His	Пe	Glu	Leu	Lys	His	Tyr	Ile	Val ,	
		370					375					380					
15																4.7.4	1200
																ATA	1200
			Leu	Asr	i Met			s Ser	116	e Arg	395		/ GIŞ	Lys		11e 400	
	385					390					330	,				400	
20	GGA	GC#	GGT	AT1	ATA	A ACA	GA/	ATA A	AA.	AA A							1230
	Gly	/ Ala	a G13	/ I1e	e Ile	e Thr	- G1	ı Ile	Lys	s Asr	ì						
					40					410							
25	(2)) IN	FORM	ATIO	N FO	R SE	Q ID	NO:	2:								
										_							
						E CH											
						TH:				ıas							
20						: am LOGY											
30				(U)	IUFU	LOGI	. ''	icui									

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

	Met 1	Asn	Asn	Lys	Leu 5	Phe	Leu	Arg	Asn	Lys 10	G1n	His	Ile	Asn	Leu 15	G1y
5	Thr	Ile	Gly	His 20	Val	Asp	His	Gly	Lys 25	Thr	Thr	Leu	Thr	Thr 30	Ala	Ile
10	Ser	Tyr	Leu 35	Leu	Asn	Leu	G1n	G1y 40	Leu	Ser	Lys	L y s	Tyr 45	Asn	Tyr	Ser
	Asp	I1e 50	Asp	Ser	Ala	Pro	G1u 55	G1 u	Lys	Ile	Arg	Gly 60	Ile	Thr	Ile	Asn
15	Thr 65		His	Ile	Glu	Tyr 70	Glu	Thr	Leu	Thr	Lys 75	His	Cys	Ala	His	Ile 80
	Asp	Cys	Pro	G1 y	His 85		Asp	Tyr	Ile	Lys 90		Met	Ile	Ile	G1 y 95	Ala
20	Thr	- Glr	Met	Asp		Ala	Ile	Leu	Val 105		Ser	Ile	Ile	Asp	Gly	Ile
25	Met	: Pro	Gln 115		· Tyr	- G1u	His	Leu 120		Leu	ı Ile	Lys	Gln 125		G1 y	Ile
	Lys	130	n Ile	: Ile	e Ile	Phe	Leu 135		ı Lys	G]ı	ı Asp	Leu 140		Asp	Asp	Val
30	G1:		u Il∈	e Ası	o Phe	11e		s Leu	ı G1u	u Va ⁻	1 Asr		. Leu	. Leu	ı Ile	Lys 160

	Tyr	Asn	Phe		Leu / 165	Asn	ıyr	11e		170	Leu	i nr	ыу	ser.	175	Leu
5	Asn	Val	Ile	Asn 180	Ile	Ile (Gln		Asn 185	Lys	Asp	Tyr	Glu	Leu 190	Ile	Lys
	Ser	Asn	Ile 195	Trp	Ile	Gln	Lys	Leu 200	Asn	Asn	Leu	Ile	G1n 205	Ile	Ile . :	Asp
10	Asn	Ile 210	Ile	Ile	Pro		Arg 215	Lys	Ile	Asn	Asp	Tyr 220	Phe	Leu	Met	Ser
1.5	Ile 225	Glu	Asp	Val	Phe	Ser 230	Ile	Thr	Gly	Arg	G1 y 235	Thr	Val	Val	Thr	Gly 240
15	Lys	Ile	G1u	Gln	Gly 245	Cys	Ile	Asn	Leu	Asn 250	Asp	G1u	Ile	Glu	Ile 255	Leu
20	Lys	Phe	G1u	Lys 260	Ser	Ser	Pro	Asn	Leu 265		Thr	Val	Ile	G1 y 270		G1u
	Met	. Phe	275		G1n	Leu	Thr	G1n 280		G1n	Ser	Gly	Asp 285		ı Val	Gly
25	Ile	290		u Arç	j Asn	Ile	G1r 295		Lys	Asp	· Ile	300		g Gly	/ Met	: Ile
30	Let 305		a Thi	r Pro	o Asr	1 Lys 310		ı Lys	s Val	l Tyr	Lys 315		r Phe	e Ile	e Ala	320
	Thi	r Ty	r Il	e Le	u Thr		G1:	u G1	u G1	y G1:		g Hi:	s Ly	s Pr	o Phe	e Asn

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Ile Gly Tyr Lys Pro Gln Phe Phe Ile Arg Thr Val Asp Val Thr Gly $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350$

Glu Ile Lys Asn Ile Tyr Leu Asn Glu Asn Val Gln Lys Val Ala Ile 355 360 365

Pro Gly Asp Lys Ile Thr Leu His Ile Glu Leu Lys His Tyr Ile Val $370 \hspace{1cm} 375 \hspace{1cm} 380$

10 Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile 385 390 395 400

Gly Ala Gly Ile Ile Thr Glu Ile Lys Asn 405 410